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APR 01 2002

TECH CENTER 1600/2900

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/974,592

DATE: 03/08/2002 P.5  
TIME: 14:09:04

Input Set : A:\07891.009004.SEQLIST.TXT

Output Set: N:\CRF3\03082002\I974592.raw

4 <110> APPLICANT: Korneluk, Robert G  
5 MacKenzie, Alexander E  
6 Liston, Peter  
7 Baird, Stephen  
8 Tsang, Benjamin K  
9 Pratt, Christine  
11 <120> TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
12 NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
13 DISEASE  
15 <130> FILE REFERENCE: 07891/009004  
17 <140> CURRENT APPLICATION NUMBER: US 09/974,592  
18 <141> CURRENT FILING DATE: 2001-10-09  
20 <150> PRIOR APPLICATION NUMBER: US 09/617,053  
21 <151> PRIOR FILING DATE: 2000-07-14  
23 <150> PRIOR APPLICATION NUMBER: US 08/800,929  
24 <151> PRIOR FILING DATE: 1997-02-13  
26 <160> NUMBER OF SEQ ID NOS: 17  
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
30 <210> SEQ ID NO: 1  
31 <211> LENGTH: 46  
32 <212> TYPE: PRT  
33 <213> ORGANISM: Artificial Sequence  
35 <220> FEATURE:  
36 <221> NAME/KEY: VARIANT  
37 <222> LOCATION: (1)...(46)  
38 <223> OTHER INFORMATION: Xaa at 2, 3, 4, 5, 6, 7, 9, 10, 11, 17, 18, 19,  
39 20, 21, 23, 25, 30, 31, 32, 34, 35, 38, 39, 40,  
40 41, 42, and 45 can be any amino acid; Xaa at 8 can  
41 be Glu or Asp; Xaa at 14 and 22 can be Val or Ile.  
43 <223> OTHER INFORMATION: Based on consensus from Homo sapiens and Mus  
44 musculus  
46 <400> SEQUENCE: 1  
W--> 47 Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Lys Xaa Cys Met  
48 1 5 10 15  
W--> 49 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Pro Cys Gly His Xaa Xaa Xaa  
50 20 25 30  
W--> 51 Cys Xaa Xaa Cys Ala Xaa Xaa Xaa Xaa Xaa Cys Pro Xaa Cys  
52 35 40 45  
55 <210> SEQ ID NO: 2  
56 <211> LENGTH: 68  
57 <212> TYPE: PRT  
58 <213> ORGANISM: Artificial Sequence  
60 <220> FEATURE:

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Output Set: N:\CRF3\03082002\I974592.raw

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61 <221> NAME/KEY: VARIANT
62 <222> LOCATION: (1)...(68)
63 <223> OTHER INFORMATION: Xaa at 1, 2, 3, 6, 9, 10, 14, 15, 18, 19, 20, 21,
64      24, 30, 32, 33, 35, 37, 40, 42, 43, 44, 45, 46,
65      47, 49, 50, 51, 53, 54, 55, 56, 57, 59, 60, 61,
66      62, 64 and 66 can be any amino acid; Xaa at 13, 16
W--> 67      and 17 can be any amino acid or absent.
69 <223> OTHER INFORMATION: Based on consensus from Homo sapiens and Mus
70      musculus
73 <400> SEQUENCE: 2
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75      1          5          10          15
W--> 76 Xaa Xaa Xaa Xaa Xaa Leu Ala Xaa Ala Gly Phe Tyr Tyr Xaa Gly Xaa
77      20          25          30
W--> 78 Xaa Asp Xaa Val Xaa Cys Phe Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp
79      35          40          45
W--> 80 Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Pro Xaa
81      50          55          60
W--> 82 Cys Xaa Phe Val
83      65
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87 <211> LENGTH: 5232
88 <212> TYPE: DNA
89 <213> ORGANISM: Homo sapiens
91 <220> FEATURE:
92 <221> NAME/KEY: variation
93 <222> LOCATION: 4623
94 <223> OTHER INFORMATION: n can be any nucleotide
96 <221> NAME/KEY: variation
97 <222> LOCATION: 4622
98 <223> OTHER INFORMATION: n can be any nucleotide
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102 aaaacttggtg tacctgcaga catcaataag gaagaagaat ttgtagaaga gtttaataga 120
103 ttaaaaactt ttgctaattt tccaagtggg agtctgtttt cagcatcaac actggcacga 180
104 gcagggtttc ttataactgg tgaaggagat accgtgcggg gctttagttg tcatgcagct 240
105 gtagatagat ggcaatatgg agactcagca gttggaagac acaggaaagt atccccaaat 300
106 tgcagattta tcaacggctt ttatcttgaa aatagtgcc cgcagtctac aaattctggg 360
107 atccagaatg gtcagtacaa agttgaaaac tatctgggaa gcagagatca ttttgctta 420
108 gacaggccat ctgagacaca tgcagactat cttttgagaa ctgggcaggg ttagatatata 480
109 tcagacacca tatacccgag gaacctgcc atgtatagtg aagaagctag attaaagtcc 540
110 tttcagaact ggccagacta tgctcaccta accccaagag agttagcaag tgctggactc 600
111 tactacacag gtattggtga ccaagtgcag tgcttttgtt gtggtggaaa actgaaaaat 660
112 tgggaacctt gtgatcgtgc ctggtcagaa cacaggcgac actttcctaa ttgcttcttt 720
113 gttttggggc ggaatcttaa tattcgaagt gaatctgatg ctgtgagttc tgataggaat 780
114 ttcccaaat caacaaatct tccaagaaat ccatccatgg cagattatga agcacggatc 840
115 tttacttttg ggacatggat ataactcagtt aacaaggagc agcttgcaag agctggattt 900
116 tatgcttttag gtgaagggtga taaagtaaag tgcttttact gtggaggagg gctaactgat 960
117 tggaaagccca gtgaagaccc ttgggaacaa catgctaaat ggtatccagg gtgcaaatat 1020

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```

118 ctgttagaac agaagggaca agaatatata aacaatatc atttaactca ttcacttgag 1080
119 gagtgtctgg taagaactac tgagaaaaca ccatcactaa ctagaagaat tgatgatacc 1140
120 atcttccaaa atcctatggt acaagaagct atacgaatgg gggttcagttt caaggacatt 1200
121 aagaaaaataa tggaggaaaa aattcagata tctgggagca actataaatc acttgagggtt 1260
122 ctggttgacg atctagtga tgcacagaaa gacagtatgc aagatgagtc aagtcagact 1320
123 tcattacaga aagagattag tactgaagag cagctaaggc gcctgcaaga ggagaagctt 1380
124 tgcaaaatct gtatggatag aaatattgct atcgtttttg ttccttgagg acatctagtc 1440
125 acttgtaaac aatgtgctga agcagttgac aagtgtccca tgtgctacac agtcattact 1500
126 ttcaagcaaa aaatttttat gtcttaattc aactctatag taggcatggt atgttggttct 1560
127 tattaccctg attgaatgtg tgatgtgaac tgactttaag taatcaggat tgaattccat 1620
128 tagcatttgc taccaagtag gaaaaaaaat gtacatggca gtgttttagt tggcaatata 1680
129 atctttgaat ttcttgattt ttcagggtat tagctgtatt atccattttt tttactgtta 1740
130 ttttaattgaa accatagact aagaataaga agcatcatac tataactgaa cacaatgtgt 1800
131 attcatagta tactgattta atttctaagt gtaagtgaat taatcatctg gattttttat 1860
132 tcttttcaga taggcttaac aaatggagct ttctgtatat aaatgtggag attagagtta 1920
133 atctccccaa tcacataatt tgttttgtgt gaaaaaggaa taaattgttc catgctggtg 1980
134 gaaagataga gattgttttt agaggttggt tgttggtgtt taggattctg tccattttct 2040
135 tttaaagtta taaacacgta cttgtgcgaa ttattttttt aaagtgattt gccatttttg 2100
136 aaagcgtatt taactgata atactatcga gccaacatgt actgacatgg aaagatgtca 2160
137 aagatatggt aagtgtaaaa tgcaagtggc aaaacactat gtatagtctg agccagatca 2220
138 aagtatgtat gtttttaata tgcatagaac aaaagatttg gaaagatata caccaaaactg 2280
139 ttaaagtgtg tttctcttcg gggagggggg gattggggga ggggccccag aggggtttta 2340
140 taggggacct ttcactttct acttttttca ttttgttctg ttcgaatttt ttataagtat 2400
141 gtattacttt tgtaatcaga attttttaga agtattttgc tgatttaaag gcttaggcat 2460
142 gttcaaacgc ctgcaaaact acttatcact cagcttttagt ttttctaata caagaaggca 2520
143 gggcagttaa cttttttggt gccaatgtga aatgtaaatg attttatgtt tttcctgctt 2580
144 tgtggatgaa aaatatttct gagtggtagt ttttgacag gtagaccatg tcttatcttg 2640
145 tttcaaaata agtatttctg attttgtaaa atgaaatata aaatatgtct cagatcttcc 2700
146 aattaattag taaggattca tccttaatcc ttgctagttt aagcctgcct aagtcacttt 2760
147 actaaaagat ctttgttaac tcagtatttt aaacatctgt cagcttatgt aggtaaaagt 2820
148 agaagcatgt ttgtacactg cttgtagtta tagtgacagc tttccatgtt gagattctca 2880
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150 ataggacaaa atgttaagtc tttcctctac ctacatttgt tttcttggtc agtaatagta 3000
151 gtagatactt ctgaaataaa tgttctctca agatccttaa aacctcttgg aaattataaa 3060
152 aatattggca agaaaagaag aatagttggt taaatatttt ttaaaaaaca cttgaataag 3120
153 aatcagtagg gtataaacta gaagtttaaa aatgcctcat agaacgtcca gggtttacat 3180
154 tacaagattc tcacaacaaa cccattgtag aggtgagtaa ggcatgttac tacagaggaa 3240
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156 ttgttatgtt ctccaaactt ctggtgatta ctactttaag tgatattcat ttaaaacatt 3360
157 gcaaatttat tttatttatt taattttctt tttgagatgg agtcttgctt gtcaccagag 3420
158 ctggagtgca gtggagtgat ctctgctcac tgcaacctcc gccttctggg ttcaagcgat 3480
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161 tctgacctc aagagatcca ctgccttgc cctcccaaag tgcgtgggatt acaggcttga 3660
162 gccaccacgc ccggctaaaa cattgcaaat ttaaatgaga gttttaaaaa ttaataatg 3720
163 actgccctgt ttctgtttta gtatgtaaat cctcagttct tcacctttgc actgtctgcc 3780
164 acttagtttg gttatatagt cattaacttg aatttggctt gtatagtota gactttaaat 3840
165 ttaaagtttt ctacaagggg agaaaagtgt taaaattttt aaaatatgtt ttccaggaca 3900
166 cttcacttcc aagtcaggta ggtagttcaa tctagttgtt agccaaggac tcaaggactg 3960

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167 aattgtttta acataaggct tttcctgttc tgggagccgc acttcattaa aattcttcta 4020
168 aaacttgtat gtttagagtt aagcaagact ttttttcttc ctctccatga gttgtgaaat 4080
169 ttaatgcaca acgctgatgt ggctaacaag tttatttttaa gaattgttta gaaatgctgt 4140
170 tgcttcaggt tcttaaaatc actcagcact ccaacttcta atcaaat tttt tgggagactta 4200
171 acagcatttg tctgtgtttg aactataaaa agcaccggat cttttccatc taattccgca 4260
172 aaaattgata atttgcaaag tcaaaactat agccatatcc aaatcttttc cccctcccaa 4320
173 gagttctcag tgtctacatg tagactattc cttttctgta taaagttcac tctaggattt 4380
174 caagtcacca cttattttac attttagtca tgcaaagatt caagtagttt tgcaataagt 4440
175 acttatcttt atttgtaata atttagtctg ctgatcaaaa gcattgtctt aatttttgag 4500
176 aactggtttt agcatttaca aactaaattc cagttaatta attaatagct ttatattgcc 4560
177 tttcctgcta catttggttt tttccctgtt ccctttgatt acggggctaag gtagggtaag 4620
W--> 178 annnggtgta gtgagtgtat ataattgtgat ttggccctgt gtattatgat attttgttat 4680
179 ttttgttgtt atattattta catttcagta gttgtttttt gtgtttccat tttaggggat 4740
180 aaaatttgta ttttgaacta tgaatggaga ctaccgcccc agcattagtt tcacatgata 4800
181 taccctttta acccgaatca ttgttttatt tcctgattac acaggtgttg aatggggaaa 4860
182 ggggctagta tatcagtagg atatactatg ggatgtatat atatcattgc tgtagagaaa 4920
183 atgaaataaa atggggctgg gctcagtggc tcacgcctgt aatcccagca ctttgggagg 4980
184 ctgaggcagg tggatcacga ggtcaggaga tcgagaccat cctggctaac acggtgaaac 5040
185 cccgtctcta ctaaaaaaca gaaaattagc cgggcggtgg ggcgggcgcc tgtagtcca 5100
186 gctactcggg aggctgaggc aggagaatgg tgtgaaccgc ggaggcagag cttgcagtga 5160
187 gccgagatct cgccactgca ctccagcctg ggcaacagag caagactctg tctcaaaaaa 5220
188 aaaaaaaaaa ag 5232
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 497
192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 4
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197 1 5 10 15
198 Ile Asn Lys Glu Glu Glu Phe Val Glu Glu Phe Asn Arg Leu Lys Thr
199 20 25 30
200 Phe Ala Asn Phe Pro Ser Gly Ser Pro Val Ser Ala Ser Thr Leu Ala
201 35 40 45
202 Arg Ala Gly Phe Leu Tyr Thr Gly Glu Gly Asp Thr Val Arg Cys Phe
203 50 55 60
204 Ser Cys His Ala Ala Val Asp Arg Trp Gln Tyr Gly Asp Ser Ala Val
205 65 70 75 80
206 Gly Arg His Arg Lys Val Ser Pro Asn Cys Arg Phe Ile Asn Gly Phe
207 85 90 95
208 Tyr Leu Glu Asn Ser Ala Thr Gln Ser Thr Asn Ser Gly Ile Gln Asn
209 100 105 110
210 Gly Gln Tyr Lys Val Glu Asn Tyr Leu Gly Ser Arg Asp His Phe Ala
211 115 120 125
212 Leu Asp Arg Pro Ser Glu Thr His Ala Asp Tyr Leu Leu Arg Thr Gly
213 130 135 140
214 Gln Val Val Asp Ile Ser Asp Thr Ile Tyr Pro Arg Asn Pro Ala Met
215 145 150 155 160
216 Tyr Cys Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr
217 165 170 175

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218 Ala His Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr
219          180          185          190
220 Gly Ile Gly Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys
221          195          200          205
222 Asn Trp Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe
223          210          215          220
224 Pro Asn Cys Phe Phe Val Leu Gly Arg Asn Leu Asn Ile Arg Ser Glu
225          225          230          235          240
226 Ser Asp Ala Val Ser Ser Asp Arg Asn Phe Pro Asn Ser Thr Asn Leu
227          245          250          255
228 Pro Arg Asn Pro Ser Met Ala Asp Tyr Glu Ala Arg Ile Phe Thr Phe
229          260          265          270
230 Gly Thr Trp Ile Tyr Ser Val Asn Lys Glu Gln Leu Ala Arg Ala Gly
231          275          280          285
232 Phe Tyr Ala Leu Gly Glu Gly Asp Lys Val Lys Cys Phe His Cys Gly
233          290          295          300
234 Gly Gly Leu Thr Asp Trp Lys Pro Ser Glu Asp Pro Trp Glu Gln His
235          305          310          315          320
236 Ala Lys Trp Tyr Pro Gly Cys Lys Tyr Leu Glu Gln Lys Gly Gln
237          325          330          335
238 Glu Tyr Ile Asn Asn Ile His Leu Thr His Ser Leu Glu Glu Cys Leu
239          340          345          350
240 Val Arg Thr Thr Glu Lys Thr Pro Ser Leu Thr Arg Arg Ile Asp Asp
241          355          360          365
242 Thr Ile Phe Gln Asn Pro Met Val Gln Glu Ala Ile Arg Met Gly Phe
243          370          375          380
244 Ser Phe Lys Asp Ile Lys Lys Ile Met Glu Glu Lys Ile Gln Ile Ser
245          385          390          395          400
246 Gly Ser Asn Tyr Lys Ser Leu Glu Val Leu Val Ala Asp Leu Val Asn
247          405          410          415
248 Ala Gln Lys Asp Ser Met Gln Asp Glu Ser Ser Gln Thr Ser Leu Gln
249          420          425          430
250 Lys Glu Ile Ser Thr Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys
251          435          440          445
252 Leu Cys Lys Ile Cys Met Asp Arg Asn Ile Ala Ile Val Phe Val Pro
253          450          455          460
254 Cys Gly His Leu Val Thr Cys Lys Gln Cys Ala Glu Ala Val Asp Lys
255          465          470          475          480
256 Cys Pro Met Cys Tyr Thr Val Ile Thr Phe Lys Gln Lys Ile Phe Met
257          485          490          495
258 Ser
262 <210> SEQ ID, NO: 5
263 <211> LENGTH: 6669
264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
267 <220> FEATURE:
268 <221> NAME/KEY: variation
269 <222> LOCATION: (3677)...(3951)
270 <223> OTHER INFORMATION: n can be any nucleotide

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

DATE: 03/08/2002

PATENT APPLICATION: US/09/974,592

TIME: 14:09:05

Input Set : A:\07891.009004.SEQLIST.TXT

Output Set: N:\CRF3\03082002\I974592.raw

L:47 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:67 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5